



GENERAL INFORMATION:  
 APPLICANT: HENRY, JAMES  
 APPLICANT: CAHILL, CATHERINE  
 APPLICANT: YASHPAL, KIRAN  
 TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
 TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
 FILE REFERENCE: 39245-173913  
 CURRENT APPLICATION NUMBER: US/09/930,503  
 CURRENT FILING DATE: 2001-08-16  
 PRIOR APPLICATION NUMBER: 60/226,086  
 PRIOR FILING DATE: 2000-08-18  
 SEQ ID NO: 59  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 311  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-930-503-3

Query Match 100.0%; Score 114; DB 10; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-10; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0;  
 .Qy 1 NYFLVNLAFAEASMAAFNTVNF 23  
 Db 68 NYFLVNLAFAEASMAAFNTVNF 90

RESULT 3  
 US-09-930-503-5  
 Sequence 5, Application US/09930503  
 Publication No. US20030066438A1.  
 GENERAL INFORMATION:  
 APPLICANT: HENRY, JAMES  
 APPLICANT: CAHILL, CATHERINE  
 APPLICANT: YASHPAL, KIRAN  
 TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
 TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
 FILE REFERENCE: 39245-173913  
 CURRENT APPLICATION NUMBER: US/09/930,503  
 CURRENT FILING DATE: 2001-08-16  
 PRIOR APPLICATION NUMBER: 60/226,086  
 PRIOR FILING DATE: 2000-08-18  
 NUMBER OF SEQ ID NO: 59  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 5  
 LENGTH: 407  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-930-503-5

Query Match 100.0%; Score 114; DB 10; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-10; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0;

RESULT 4  
 US-09-930-503-7  
 Sequence 7, Application US/09930503  
 Publication No. US2003006438A1.  
 GENERAL INFORMATION:  
 APPLICANT: HENRY, JAMES  
 APPLICANT: CAHILL, CATHERINE  
 APPLICANT: YASHPAL, KIRAN  
 TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
 TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
 FILE REFERENCE: 39245-173913  
 CURRENT APPLICATION NUMBER: US/09/930,503  
 CURRENT FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 60/226,086  
 PRIORITY FILING DATE: 2000-08-18  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 7  
 LENGTH: 407  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-930-503-7

Query Match 100.0%; Score 114; DB 10; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-10; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0;  
 .Qy 1 NYFLVNLAFAEASMAAFNTVNF 23  
 Db 68 NYFLVNLAFAEASMAAFNTVNF 90

RESULT 5  
 US-09-926-509-525  
 Sequence 525, Application US/09826509  
 Publication No. US20030204073A1.  
 GENERAL INFORMATION:  
 APPLICANT: Lehmann-Bruinsma, Karin  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lin, I-Lin  
 TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G Protein-Coupled Receptors  
 FILE REFERENCE: ALEN-207  
 CURRENT APPLICATION NUMBER: US/09/826,509  
 CURRENT FILING DATE: 2001-04-05  
 PRIORITY APPLICATION NUMBER: 60/1195,747  
 PRIOR FILING DATE: 2000-04-07  
 PRIORITY APPLICATION NUMBER: 09/170,496  
 PRIOR FILING DATE: 1998-10-13  
 NUMBER OF SEQ ID NOS: 589  
 SOFTWARE: PatentIn Version 2.1  
 SEQ ID NO 525  
 LENGTH: 407  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-926-509-525

Query Match 100.0%; Score 114; DB 10; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-10; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0;

RESULT 6  
 US-10-005-956-14  
 Sequence 14, Application US/10005956  
 Publication No. US2003011372A1.  
 GENERAL INFORMATION:  
 APPLICANT: Bristol-Myers Squibb Company  
 TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
 FILE REFERENCE: D0053NP  
 CURRENT APPLICATION NUMBER: US/10/005,956  
 CURRENT FILING DATE: 2001-12-03  
 PRIORITY APPLICATION NUMBER: 60/251,015  
 PRIOR FILING DATE: 2000-12-04  
 PRIORITY APPLICATION NUMBER: 60/263,678  
 PRIOR FILING DATE: 2001-01-23  
 PRIORITY APPLICATION NUMBER: 60/273,037  
 PRIOR FILING DATE: 2001-03-02  
 NUMBER OF SEQ ID NOS: 1579  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 14  
 LENGTH: 407



Query Match 100.0%; Score 114; DB 14; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 68 NYFLVNLAFAEASMAAFNTVNF 90

RESULT 13  
 US-10-254-905-8  
 ; Sequence 8, Application US/10254905  
 ; Publication No. US20030186265A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBNY7, EXPRESSED HIGHLY IN SPINAL CORD  
 ; FILE REFERENCE: D0044 CIP  
 ; CURRENT APPLICATION NUMBER: US/10/254,905  
 ; CURRENT FILING DATE: 2002-09-25  
 ; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 410  
 ; TYPE: PRT  
 ; ORGANISM: CHICKEN  
 ; US-10-254-905-8

Query Match 97.4%; Score 111; DB 14; Length 410;  
 Best Local Similarity 95.7%; Pred. No. 2.7e-09;  
 Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 NYFLVNLAFAEASMAAFNTVNF 23  
 Db 72 NYFLVNLAFAEASMAAFNTVNF 94

RESULT 14  
 US-09-966-782A-8  
 ; Sequence 8, Application US/09966782A  
 ; Publication No. US20030022183A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Battaglino, P.  
 ; APPLICANT: Feder, J. N.  
 ; APPLICANT: Mintier, G.  
 ; APPLICANT: Ramanathan, C. S.  
 ; APPLICANT: Westphal, R.  
 ; APPLICANT: Hawken, D. R.  
 ; APPLICANT: Barber, L.  
 ; APPLICANT: Kornacker, M. G.  
 ; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBNY7,  
 ; EXPRESSED HIGHLY IN SPINAL CORD  
 ; FILE REFERENCE: D0044NP  
 ; CURRENT APPLICATION NUMBER: US/09/966,782A  
 ; CURRENT FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: 60/1235,731  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: 60/268,580  
 ; PRIOR FILING DATE: 2001-02-14  
 ; PRIOR APPLICATION NUMBER: 60/315,423  
 ; PRIOR FILING DATE: 2001-08-28  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 411  
 ; TYPE: PRT  
 ; ORGANISM: CHICKEN  
 ; US-09-966-782A-8

Query Match 97.4%; Score 111; DB 10; Length 411;  
 Best Local Similarity 95.7%; Pred. No. 2.7e-09;  
 Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 NYFLVNLAFAEASMAAFNTVNF 23  
 Db 72 NYFLVNLAFAEASMAAFNTVNF 94

Query Match 100.0%; Score 114; DB 17; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 68 NYFLVNLAFAEASMAAFNTVNF 23

RESULT 15  
 US-09-443-745-20  
 Sequence 20, Application US/09443745  
 Publication No. US20030055218A1  
 GENERAL INFORMATION:  
 APPLICANT: WANK, Stephen A.  
 TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF  
 TITLE OF INVENTION: CHOLICYSTOKININ RECEPTOR-ENCODING DNA  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 1800 Diagonal Road, Suite 500  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/443,745  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/029,170  
 FILING DATE: 10-MAR-1993  
 APPLICATION NUMBER: US 07/937,609  
 FILING DATE: 02-SEP-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/928,033  
 FILING DATE: 11-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/861,769  
 FILING DATE: 01-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/831,248  
 FILING DATE: 07-FEB-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 40399/166 NIH  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-9100  
 TELEFAX: (703) 683-4109  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 372 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: rat substance P receptor  
 US-09-443-745-20

Query Match 95.6%; Score 109; DB 10; Length 372;  
 Best Local Similarity 95.7%; Pred. No. 5e-09;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 NYFLVNLAFAEASMAAFNTVNF 23  
 Db 68 NYFLVNLAFAEACMAAFNTVNF 90

Search completed: April 19, 2005, 14:47:54  
 Job time : 52 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	23	6 ADB16907	Adb16907 Human neu
2	114	100.0	29	6 ADB16907	Adb16907 Human neu
3	114	100.0	311	2 AAR28800	Aar28800 Human neu
4	114	100.0	311	5 AAU91342	Aau91342 Neurokini
5	114	100.0	407	2 AAR27524	Aar27524 Human rec
6	114	100.0	407	2 AAR25306	Aar25306 hsp90ats2
7	114	100.0	407	2 AAR32799	Aar32799 Substance
8	114	100.0	407	4 ABB56366	Abb56366 Non-endog
9	114	100.0	407	5 ABG76988	Abg76988 Human tac
10	114	100.0	407	5 ABG76987	Abg76987 Human tac
11	114	100.0	407	5 ABG76987	Abg76987 Human tac
12	114	100.0	407	5 ABG76989	Abg76989 Human tac
13	114	100.0	407	5 AAGU77000	Aag77000 Human tac
14	114	100.0	407	5 AAU91345	Aau91345 Neurokini
15	114	100.0	407	5 AAU91344	Aau91344 Neurokini
16	114	100.0	407	5 AAU78238	Aau78238 Human Tac
17	114	100.0	407	5 ABB99006	Abb99006 Mutant hu
18	114	100.0	407	6 ABB81918	Abb81918 Human tac
19	114	100.0	407	8 ADO29656	Ado29656 Human GPC
20	109	95.6	372	4 AAB66623	Aab66623 Rat subst
21	109	95.6	407	4 AAR12970	Aar12970 Substance
22	109	95.6	407	2 AAR32800	Aar32800 Rat Subst
23	109	95.6	407	8 ADO29657	Ado29657 Mouse GPC
24	105	92.1	415	8 ABM83920	Abm83920 Human dia
25	105	92.1	465	2 AAR41973	Aar41973 Human neu

factors. The penetrating peptide is useful for the treatment of various conditions including diabetes, infertility, hormone and vitamin deficiencies, neurodegenerative, cardiovascular, haematological and endocrine disorders, as well as obesity and neoplastic disease. Accordingly, the peptides of this invention can be used in compositions that have neuroprotective, cardiant, antiarteriosclerotic, osteopathic, cytostatic or nootropic activities. This Peptides is from the human neurokinin 1 (NK-1) receptor and is penetrating peptide 29 of the invention.

Sequence 23 AA;

Query Match 100.0%; Score 114; DB 6; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAPEASMAAFNTVNF 23  
 Db 1 NYFLVNLAPEASMAAFNTVNF 23

RESULT 2  
 ADB16917 standard / peptide; 29 AA.  
 AC ADB16917;  
 XX 20-NOV-2003 (first entry)  
 XX Escherichia coli Peptide 3 coupled to imaging compound linker, IBW-007.  
 KW epithelial; endothelial; tight junction; diabetes; infertility; hormone;  
 KW vitamin deficiency; neurodegenerative; cardiovascular; haematological;  
 KW endocrine disorder; obesity; neoplastic disease; neuroprotective;  
 KW cardiant; antiarteriosclerotic; osteopathic; cytostatic; nootropic;  
 KW imaging linker; penetrating peptide; IBW-007.  
 XX Synthetic.  
 OS Escherichia coli.

Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetyl"  
 FT Modified-site 29 /note= "C-terminal amide"

WO2003066859-A2.

PN 14-AUG-2003.

F1 07-FEB-2003; 2003WO-IB000968.

F1 07-FEB-2002; 2002US-0355396P.

(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

P1 Ben-Sasson SA, Cohen E;

XX WPI; 2003-697452/66.

XX New penetrating peptide, useful for preparing a composition for treating

PT or preventing e.g. endocrine disorders.

PS Example 3; Page 40; 60pp; English.  
 XX This invention relates to a novel peptide sequences capable of

CC translocating across a biological barrier. Furthermore, it refers to  
 CC methods that use these peptides to facilitate penetration of a  
 CC biologically active effector molecule such as a drug or other therapeutic  
 CC agent across biological barriers e.g. epithelial or endothelial cells  
 CC sealed by tight junctions. This peptide is derived from a bacterial  
 CC toxin, an integral membrane or extracellular protein and can comprise an  
 CC anticoagulant, antibiotic, antipathogenic agent, immunomodulator, vitamin

or enzyme. The effector molecule, however, can comprise for example insulin, gonadotropin, erythropoietin, granulocyte/monocyte colony stimulating factor (GM-CSF), eukalpulin, dalfargin, or neurotrophic factors. The penetrating peptide is useful for the treatment of various conditions including diabetes, infertility, hormone and vitamin deficiencies, neurodegenerative, cardiovascular, haematological and endocrine disorders, as well as obesity and neoplastic disease. Accordingly, the peptides of this invention can be used in compositions that have neuroprotective, cardiant, antiarteriosclerotic, osteopathic, cytostatic or nootropic activities. This Peptide sequence is IBW-007, which consists of the Escherichia coli Penetrating Peptide 3 coupled to the imaging linker peptide used in an exemplification of the invention.

XX Sequence 29 AA;  
 SQ Query Match 100.0%; Score 114; DB 6; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 NYFLVNLAPEASMAAFNTVNF 23  
 Db 1 NYFLVNLAPEASMAAFNTVNF 23

RESULT 3

AAR28800

ID AAR28800 standard; protein; 311 AA.

XX AC AAR28800;

XX DT 25-MAR-2003 (revised)

DT 22-MAR-1993 (first entry)

XX DB Human neurokinin-1 receptor.

XX KW NK1R sF; arthritis; Substance P.

XX Homo sapiens.

OS XX EP514207-A2.

XX PN 19-NOV-1992.

XX PR 15-MAY-1992; 92EP-00304432.

XX PR 17-MAY-1991; 91US-00701930.

XX PR 17-MAY-1991; 91US-00701945.

XX PR 17-MAY-1991; 91US-00701937.

XX (MERI ) MERCK &amp; CO INC.

XX PI Strader CD, Fong TM;

XX DR WPI; 1992-384034/47.

DR N-PSDB; AAQ0557.

XX New human neurokinin-1 receptor short form protein - useful for PT identifying and determining substance P antagonists in arthritic patients.

XX Claim 3; Fig 1; 36pp; English.

CC Human neurokinin-1 receptor short form protein can be used to identify CC and evaluate ligands which bind to the receptor. The NK1 sF protein is CC suitable for use in an assay of substance P antagonists in arthritis CC patients. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 311 AA;

Query Match 100.0%; Score 114; DB 2; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





CC sequence analysis. One cDNA was isolated after restriction with HindIII  
 CC and BamHI (present in the PBS polylinker) and made blunt ended with  
 CC Klenow, as was pM2 after BamHI digestion. The cDNA was ligated to pM2 and  
 CC used to transform E. coli XL-1 Blue cells by electroporation. (Updated on  
 CC 25-MAR-2003 to correct PN field.)

XX SQ Sequence 407 AA;

Query Match 100.0%; Score 114; DB 2; Length 407;

Best Local Similarity 100.0%; Pred. No. 3.5e-10; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 0;

Qy 1 NYFLVNLAFAEASMAAFNTVYNF 23

Db 68 NYFLVNLAFAEASMAAFNTVYNF 90

RESULT 8

ID ABB55366

DE ABB55366 standard; protein; 407 AA.

XX AC ABB55366;

XX DE Non-endogenous human GPCR protein, SEQ ID NO: 525.

XX Human G protein-coupled receptor; GPCR; non-endogenous; mutant;

XX constitutively activated GPCR; agonist; disease.

XX KW Homo sapiens.

OS Synthetic.

XX PN WO200177172-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US011098.

XX PR 07-APR-2000; 2000US-0195747P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;

XX DR WPI; 2001-648759/74.

XX DR N-PSDB; ABI98002.

PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in

PT disease treatment, comprises contacting candidate compounds with versions

PT of GPCRs.

XX SQ Sequence 407 AA;

PS Claim 1; Page 326-327; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which  
 CC the endogenous ligand has been identified. Non-endogenous constitutively  
 CC activated versions of known GPCRs are used in the invention for the  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists. Such agonists are useful as  
 CC therapeutic agents for diseases or disorders associated with GPCRs. The  
 CC present sequence is a non-endogenous version of a known human GPCR  
 XX PS Query Match 100.0%; Score 114; DB 4; Length 407;

Best Local Similarity 100.0%; Pred. No. 3.5e-10; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 0;

Qy 1 NYFLVNLAFAEASMAAFNTVYNF 23

Db 68 NYFLVNLAFAEASMAAFNTVYNF 90

RESULT 9

ID ABG76988

DE ABG76988 standard; protein; 407 AA.

XX AC ABG76988;

XX DT 05-NOV-2002 (first entry)

DE Human tachykinin receptor 1 variant #1.

XX KW Aminopeptidase P; XPNEP2; bradykinin receptor B1; human; BDKRB1;

KW tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;

KW KLKL; bradykinin receptor B2; BDKRB2; gene therapy;

KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;

KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

KW cardiovascular disease; angina pectoris; hypertension; heart failure;

KW myocardial infarction; ventricular hypertrophy; vascular disease;

KW myoerythema; embolism; thrombosis; coronary artery disease; angioedema;

KW arteriosclerosis; atherosclerosis; hypertension; sepsis;

KW autoimmune disease; inflammatory arthritis; cancer; wound;

KW viral infection; bacterial infection; fungal infection; COPD;

KW Chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

XX OS Homo sapiens.

XX PN WO200261131-A2.

XX PD 08-AUG-2002.

XX XX 03-DEC-2001; 2001WO-US017235.

XX PR 04-DEC-2000; 2000US-0251015P.

XX PR 23-JAN-2001; 2001US-0261678P.

XX PR 02-MAR-2001; 2001US-0272037P.

XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PA (TSUDC/) TSUCHIHASHI Z.

XX PA (HUI/L) HUI L.

XX PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

XX PI Swanson BN, Powell JR;

XX DR 2002-619265/66.

XX WPI; 2002-619265/66.

XX DR N-PSDB; ABS59840.

XX PT New isolated nucleic acid with at least one polymorphic position, useful

XX PT for detecting, diagnosing and treating disorders such as angioedema,

XX PT cancer, viral, bacterial or fungal infection, cardiovascular and

XX PT autoimmune diseases.

XX PS Disclosure; FIG 8; 97pp; English.

XX The invention relates to an isolated nucleic acid from a human gene

CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),

CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein

CC 1 (KLKL), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme

CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one

CC polymorphic position. Also included are (1) a probe that hybridises to a

CC single nucleotide polymorphism as provided in the detailed summary of

CC nucleotide polymorphisms comprising additional 5, and 3, flanking genomic

CC sequence (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the

CC nucleic acid sequence at one or more polymorphic positions within a gene

CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids

CC ; (4), identifying (M3) an individual at risk of developing a disorder

CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor

CC using the polymorphic data; (5) a library of nucleic acids, each of which

CC comprises one or more polymorphic positions within a gene encoding a

CC human protein selected from the group above; and (6) genotyping (M4) an

CC individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at

CC least one position with a known data set. The genes, (M1, M2, M3 and M4)

and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangioma, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, heart disease, arteriosclerosis, aeurysm, thrombosis, coronary artery disease, autoimmune diseases, embolism, and/or atherosclerosis, and hypertension, heart failure, myocardial infarction, ventricular hypertrophy, heart disease, arteriosclerosis, aeurysm, thrombosis, coronary artery disease, autoimmune diseases, sepsis, autoimmunity, inflammatory arthritis, cancer, wound, viral, bacterium, fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents a polymorphic variant of one of the proteins listed above

XX

Sequence 407 AA:

Query Match 100.0%; Score 114; DB 50; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAPEASMAAFNTVNF 23  
 \*Db 68 NYFLVNLAPEASMAAFNTVNF 90

XX

RESULT 1.0

ABG76987  
 ID ABG76987 standard; protein; 407 AA.  
 XX  
 DT 05-NOV-2002 (first entry)  
 DE Human tachykinin receptor 1.

XX

Human tachykinin receptor 1.

XX

Aminopeptidase P; XPNEP2; bradykinin receptor B1; human; BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy; angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4; polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma; cardiovascular disease; angina pectoris; hypertension; heart failure; myocardial infarction; ventricular hypertrophy; vascular disease; aeurysm; embolism; thrombosis; coronary artery disease; heart failure; arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; autoimmune disease; inflammatory arthritis; cancer; wound; viral infection; bacterial infection; fungal infection; COPD; Chronic obstructive pulmonary disease; enterocolitis.

XX

Homo sapiens.

XX

W0200261131-A2.

XX

08-AUG-2002.

XX

03-DEC-2001; 2001WO-US047235.

XX

04-DEC-2000; 2000WO-US0251015P.  
 PR 23-JAN-2001; 2001US-0253678P.  
 PR 02-MAR-2001; 2001US-0273037P.

XX

(BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/ ) TSUCHIHASHI Z.  
 (HUTL/ ) HUI L.

XX  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 Swanson BN, Powell JR;

XX  
 DR WPI; 2002-619265/66.  
 DR N-PSDB; AB559839.

XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful

PT for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and autoimmune diseases.

XX

PS Disclosure; Fig 7: 977pp; English.

XX

CC The invention relates to an isolated nucleic acid from a human gene encoding an aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1), tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5', 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangioma, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polymucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents a polymorphic variant of one of the proteins listed above

SQ Sequence 407 AA:

Query Match 100.0%; Score 114; DB 50; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Query Match 100.0%; Score 114; DB 5; Length 407;

Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Query 1 NYFLVNLAPEASMAAFNTVNF 23  
 DB 68 NYFLVNLAPEASMAAFNTVNF 90

XX

RESULT 11

ID ABG76980

XX

AC ABG76980;

XX

DT 05-NOV-2002 (first entry)

XX

Human tachykinin receptor 1 variant #3.

XX

Aminopeptidase P; XPNEP2; bradykinin receptor B1; human; BDKRB1;

tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;

KLK1; bradykinin receptor B2; BDKRB2; gene therapy;

angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;

polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

cardiovascular disease; angina pectoris; hypertension; heart failure;

myocardial infarction; ventricular hypertrophy; vascular disease;

aneurysm; embolism; thrombosis; coronary artery disease; angioedema;

arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

KW

KW autoimmune disease; inflammatory arthritis; cancer; wound; viral infection; bacterial infection; fungal infection; COPD; Chronic obstructive pulmonary disease; enterocolitis.  
 XX Homo sapiens.  
 OS WO200261131-A2.  
 XX PD 08-AUG-2002.  
 XX PF 03-DEC-2001; 2001WO-US047235.  
 XX PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 XX (HUI/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH; Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR N-PSDB; ABS59842.  
 XX New isolated nucleic acid with at least one polymorphic position, useful for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and autoimmune diseases.  
 XX Disclosure: Fig 10; 977pp; English.  
 XX The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1), tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5' and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachoma, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents a polymorphic variant of one of the proteins listed above.  
 XX Sequence 407 AA;

Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 NYFLYNLAFASMAFNTVNF 23  
 Db 68 NYFLYNLAFASMAFNTVNF 90  
 RESULT 112  
 ABG75989  
 ID ABG75989 standard; protein; 407 AA.  
 XX ABG76989;  
 AC  
 XX DT 05-NOV-2002 (first entry)  
 XX Human tachykinin receptor 1 variant #2.  
 DE  
 KW Aminopeptidase P; XPNEP2; bradykinin receptor B1; human; BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;  
 KW KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 KW cardiovascular disease; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW myocardial infarction; ventricular hypertrophy; hypertension; heart failure;  
 KW aneurysm; embolism; thrombosis; vascular disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; coronary artery disease; angioedema;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic obstructive pulmonary disease; enterocolitis.  
 XX Homo sapiens.  
 OS  
 XX WO200261131-A2.  
 PN  
 XX 08-AUG-2002.  
 PR  
 XX 03-DEC-2001; 2001WO-US047235.  
 XX PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 XX (HUI/) HUI L.  
 PR  
 XX 02-MAR-2001; 2001US-0273037P.  
 PR  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 PI  
 XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI  
 XX Swanson BN, Powell JR;  
 PR  
 XX WPI; 2002-619265/66.  
 DR  
 XX N-PSDB; ABS59841.  
 PT  
 XX New isolated nucleic acid with at least one polymorphic position, useful for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and autoimmune diseases.  
 PT  
 XX Disclosure; Fig 9; 977pp; English.  
 PT  
 XX The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1), tachykinin receptor B2 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5' and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; and (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachoma, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents a polymorphic variant of one of the proteins listed above.  
 XX Sequence 407 AA;  
 PT  
 XX Query Match 100.0%; Score 114; DB 5; Length 407;

(4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcoms, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The antibodies and nucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents a polymorphic variant of one of the proteins listed above

## RESULT 1.3

K S Homo sapiens .  
K N WO200261131-A2 .  
K N 08 - AUG - 2002

X 03-DEC-2001; 2001WO-US047235.  
X 04-DEC-2000; 2000US-0251015P.  
R 23-JAN-2001; 2001US-0263678P.  
R 02-MAR-2001; 2001US-0273037P.  
X (BRIM ) BRISTOL-MYERS SQUIBB CO.  
X (TSCC ) TSUCHIMASHI Z.  
A (HULL/ ) HULL L.  
A (A ) A

XX	PI	Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
XX	PI	Swanson BN, Powell JR,
XX	PT	New isolated nucleic acid with at least one polymorphic position, useful for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and autoimmune diseases.
XX	PT	WPI; 2002-519255/66.
XX	PT	N-PSSB; ABS60104.
XX	PT	DR
XX	PT	DR
XX	PS	Disclosure; Fig 22; 977pp; English.
XX	CC	The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XNEP2), bradykinin receptor B1 (BDKRB1), calcitonin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (K1KL), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5, and 3, flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising obtaining the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids ; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor using the Polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents polymorphic variants of one of the proteins listed above
XX	SQ	Sequence 407 AA;
Qy	Query Match	100.0%; Score 114; DB 5; Length 407;
Qy	Best Local Similarity	100.0%; Pred. No. 3.5e-10;
Db	Matches 23;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	NYFLVNLAAEASMAAFNTVNF	23
68	NYFLVNLAAEASMAAFNTVNF	90

RESULT 14  
 AAU91345 ID AAU91345 standard; protein; 407 AA.  
 XX  
 AAU91345:  
 AC  
 XX DT 18-JUN-2002 (first entry)  
 XX DE Neurokinin 1 receptor (NK-1) #4.  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;



respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. AAN1342-AAN1346 represent NK-1 receptor amino acid sequences of the invention.

AA	Sequence 407 AA:	Score	DB 5;	Length	407;
Qy	Query Match	100 0%;	Score 114;	DB 5;	Length 407;
	Best Local Similarity	100 0%;	Pred. No. 3.5e-10;		
	Matches 23;	Conservative	0; Mismatches	0;	Indels 0;
					Gaps 0;
Db	1 NYFLVNLAAEASMAAANTVWPF	23			
	68 NYFLVNLAAEASMAAANTVWPF	90			

Search completed: April 19, 2005, 14:47:00  
Job time: 177 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	114	GenCore version 5.1.6	311	1	US-07-701-935-26	Sequence 26, App1
2	114	Copyright (c) 1993 - 2005 Compugen Ltd.	407	1	US-08-117-965-26	Sequence 26, App1
3	114	OM protein - protein search, using sw model	407	4	US-09-509-525	Sequence 525, App1
4	114	Run on: April 19, 2005, 14:43:54 ; Search time 47 Seconds (without alignments)	407	5	PCT-US92-06532-3	Sequence 3, App1
5	109	36.530 Million cell updates/sec	372	1	US-07-937-619-20	Sequence 20, App1
6	109	Scoring table: BL05IM62	372	3	US-08-029-170-20	Sequence 20, App1
7	109	Perfect Score: 114	372	4	US-09-443-745-20	Sequence 20, App1
8	109	Sequence: 1 NYFLVNLAAEASMAAFNTVVF 23	407	5	PCT-US92-06532-7	Sequence 7, App1
9	105	Scoring table: BL05IM62	465	3	US-08-090-369-21	Sequence 1, App1
10	105	Perfect Score: 10.0 , Gapext 0.5	465	3	US-09-482-971-1	Sequence 1, App1
11	105	Sequence: 1 NYFLVNLAAEASMAAFNTVVF 23	465	4	US-09-026-569-529	Sequence 529, App1
12	104	Scanned by: Gapext 0.5	407	2	US-08-390-000A-6	Sequence 6, App1
13	100	Scanned by: Gapext 0.5	336	1	US-08-118-270-50	Sequence 50, App1
14	100	Scanned by: Gapext 0.5	336	1	PCT-US92-08528-50	Sequence 50, App1
15	100	Scanned by: Gapext 0.5	411	3	US-07-337-609-21	Sequence 21, App1
16	100	Scanned by: Gapext 0.5	411	3	US-08-029-170-21	Sequence 21, App1
17	100	Scanned by: Gapext 0.5	411	4	US-09-443-745-21	Sequence 21, App1
18	87.7	Scanned by: Gapext 0.5	451	3	US-08-330-266A-10	Sequence 10, App1
19	85	Scanned by: Gapext 0.5	440	3	US-08-430-386A-9	Sequence 9, App1
20	79	Scanned by: Gapext 0.5	384	2	US-08-103-170-10	Sequence 10, App1
21	79	Scanned by: Gapext 0.5	387	1	US-08-196-989B-14	Sequence 14, App1
22	79	Scanned by: Gapext 0.5	387	1	US-08-160-336-14	Sequence 14, App1
23	79	Scanned by: Gapext 0.5	387	4	US-09-225-024-14	Sequence 14, App1
24	79	Scanned by: Gapext 0.5	398	4	US-09-326-569-527	Sequence 527, App1
25	78	Scanned by: Gapext 0.5	369	1	US-07-937-609-19	Sequence 19, App1
26	78	Scanned by: Gapext 0.5	369	3	US-08-029-170-19	Sequence 19, App1
27	78	Scanned by: Gapext 0.5	369	4	US-09-443-745-19	Sequence 19, App1

## ALIGNMENTS

RESULT 1  
US-07-701-935-26  
; Sequence 26, Application US/07701935  
; Patent No. 5336595

GENERAL INFORMATION:  
/ APPLICANT: Strader, C. D.  
/ FONG, T. M.  
/ TITLE OF INVENTION: Method of Using Human Neurokinin-1 Receptor Short Form  
/ NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Merck & Co., Inc.  
/ STREET: P.O. Box 2000  
/ CITY: Rahway  
/ STATE: New Jersey  
/ COUNTRY: US  
/ ZIP: 07065-0907

COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.1, Version #1.25

CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/701,935  
/ FILING DATE: 19910517  
/ CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
/ NAME: Nicholson, William H.  
/ REGISTRATION NUMBER: 25,147  
/ REFERENCE/DOCKET NUMBER: 18409

TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (908) 594-5315  
/ TELEFAX: (908) 594-4720  
/ INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
/ LENGTH: 311 amino acids  
/ TYPE: AMINO ACID  
STRANDEDNESS: Single  
TOPOLOGY: linear  
MOLECULE TYPE:  
/ US-07-701-935-26

Query Match Similarity 100.0%; Score 114; DB 1; Length 311;  
Best Local Similarity 100.0%; Pre. No. 8.8e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAAEASMAAFNTVVF 23  
Db 68 NYFLVNLAAEASMAAFNTVVF 90

RESULT 2  
 US-08-117-965-26  
 Sequence 26, Application US/08117965  
 GENERAL INFORMATION  
 APPLICANT: Tung, Fong M.  
 ATTORNEY: Cathrine, Strader D.  
 TITLE OF INVENTION: Human Neurokinin-1 Receptor  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P.O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/117,965  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 691,197  
 FILING DATE: 25-APR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholson, William H.  
 REGISTRATION NUMBER: 25,147  
 REFERENCE/DOCKET NUMBER: 18387  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-5315  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 407 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 US-08-117-965-26

Query Match 100.0%; Score 114; DB 1; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAAEASMAAFNTVNF 23  
 Db 68 NYFLVNLAAEASMAAFNTVNF 90

RESULT 3  
 US-09-826-509-525  
 Sequence 525, Application US/09826509  
 GENERAL INFORMATION  
 APPLICANT: Lehmann-Bruinsma, Karin  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lin, I-Lin  
 TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G  
 TITLE OF INVENTION: Protein-coupled Receptors

FILE REFERENCE: AREN-207  
 CURRENT APPLICATION NUMBER: US/09/826,509  
 CURRENT FILING DATE: 2001-04-05  
 PRIOR APPLICATION NUMBER: 60/195,747  
 PRIOR FILING DATE: 2000-04-07  
 PRIOR APPLICATION NUMBER: 09/170,496  
 PRIOR FILING DATE: 1998-10-13  
 NUMBER OF SEQ ID NOS: 589  
 SOFTWARE: PatentIn Version 2.1

RESULT 2  
 US-09-826-509-525  
 Sequence 525, Application US/09826509  
 GENERAL INFORMATION  
 APPLICANT: Krause, James E.  
 ATTORNEY: Krause, James E.  
 TITLE OF INVENTION: Human Substance P Receptor  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD  
 STREET: 800 N. Lindbergh Blvd.  
 CITY: St. Louis  
 STATE: Missouri  
 COUNTRY: U.S.A  
 ZIP: 63167  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/06532  
 FILING DATE: 19920805  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyer, Scott J.  
 REGISTRATION NUMBER: 25,275  
 REFERENCE/DOCKET NUMBER: 07-24 (776) A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 694-3117  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 407 amino acids  
 TYPE: amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT/US92-06532-3

Query Match 100.0%; Score 114; DB 5; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAAEASMAAFNTVNF 23  
 Db 68 NYFLVNLAAEASMAAFNTVNF 90

RESULT 4  
 PCT-US2-06532-3  
 Sequence 3, Application PC/TUS9206532  
 GENERAL INFORMATION  
 APPLICANT: Krause, James E.  
 ATTORNEY: Krause, James E.  
 TITLE OF INVENTION: Human Substance P Receptor  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD  
 STREET: 800 N. Lindbergh Blvd.  
 CITY: St. Louis  
 STATE: Missouri  
 COUNTRY: U.S.A  
 ZIP: 63167  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/06532  
 FILING DATE: 19920805  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyer, Scott J.  
 REGISTRATION NUMBER: 25,275  
 REFERENCE/DOCKET NUMBER: 07-24 (776) A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 694-3117  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 407 amino acids  
 TYPE: amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT/US92-06532-3

Query Match 100.0%; Score 114; DB 5; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAAEASMAAFNTVNF 23  
 Db 68 NYFLVNLAAEASMAAFNTVNF 90

RESULT 5  
 US-07-337-609-20  
 Sequence 20, Application US/0793769  
 GENERAL INFORMATION  
 APPLICANT: Wank, Stephen A.  
 TITLE OF INVENTION: Cloning and Functional Expression of Cholecystokinin Receptor - Encoding DNA  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/937,609  
 FILING DATE: 1992-09-02  
 CLASSIFICATION: 436  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/831,248  
 FILING DATE: 07-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/861,769  
 FILING DATE: 01-APR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 PRIOR APPLICATION NUMBER: US 07/928,033  
 FILING DATE: 11-AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 40399/166 NIH  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)836-9100  
 TELEFAX: (703) 683-4109  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 372 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: rat substance P receptor  
 US-07-937-609-20

Query Match 95.6%; Score 109; DB 1; Length 372;  
 Best Local Similarity 95.7%; Pred. No. 6.2e-09;  
 Matches 20; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 NYFLVNLAFAASMAAFNTVNF 23  
 ||||| ||||| ||||| ||||| |||||  
 Db 68 NYFLVNLAFAACMAAFNTVNF 90

RESULT 6  
 US-08-029-170-20  
 ; Sequence 20, Application US/08029170  
 ; Patent No. 6169173  
 GENERAL INFORMATION:  
 APPLICANT: WANK, Stephen A.  
 TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 1800 Diagonal Road, Suite 500  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/029,170  
 FILING DATE: 1993-03-10  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/937,609  
 FILING DATE: 02-SEP-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/928,033  
 FILING DATE: 11-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/861,769  
 FILING DATE: 01-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/831,248  
 FILING DATE: 07-FEB-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 40399/166 NIH  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)836-9100  
 TELEFAX: (703) 683-4109  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 372 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: rat substance P receptor  
 US-08-029-170-20

Query Match 95.6%; Score 109; DB 3; Length 372;  
 Best Local Similarity 95.7%; Pred. No. 6.2e-09;  
 Matches 22; Mismatches 0; Indels 1; Gaps 0;  
 Qy 1 NYFLVNLAFAASMAAFNTVNF 23  
 ||||| ||||| ||||| ||||| |||||  
 Db 68 NYFLVNLAFAACMAAFNTVNF 90

RESULT 7  
 US-09-443-745-20  
 ; Sequence 20, Application US/09443745  
 ; Patent No. 6706493  
 GENERAL INFORMATION:  
 APPLICANT: WANK, Stephen A.  
 TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 1800 Diagonal Road, Suite 500  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/443,745  
 FILING DATE:  
 CLASSIFICATION:

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||||||||| 68 NYFLVNLAFAEACMAAFNTVNF 90
Db

RESULT 9
US-08-090-369-1
; Sequence 1, Application US/08090369
; Patent No. 6258943
; GENERAL INFORMATION:
; APPLICANT: Fong, T.M.
; APPLICANT: Huang, R.R. C.
; APPLICANT: Strader, C.D.
; TITLE OF INVENTION: Human Neurokinin-3 Receptor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,369
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/851,974
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thies, J. E.
; REGISTRATION NUMBER: P-35,382
; REFERENCE/DOCKET NUMBER: 18685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-090-369-1

Query Match 95.6%; Score 109; DB 4; Length 372;
Best Local Similarity 95.7%; Pred. No. 6.2e-09
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYFLVNLAFAEACMAAFNTVNF 23
Db 68 NYFLVNLAFAEACMAAFNTVNF 90

RESULT 8
PC-US92-065312-7
Sequence 7, Application PC/TUSS206532
GENERAL INFORMATION:
APPLICANT: Krause, James E.
TITLE OF INVENTION: Human Substance P Receptor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Scott J. Meyer, Monsanto Co., A3SD
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06532
; FILING DATE: 19920805
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 407 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PC-US92-065312-7

Query Match 95.6%; Score 109; DB 5; Length 407;
Best Local Similarity 95.7%; Pred. No. 6.8e-09
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NYFLVNLAFAEACMAAFNTVNF 23

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COUNTRY: USA  
 ZIP: 07065-0007  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/482,971  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/090,369  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Thies, J. E.  
 REGISTRATION NUMBER: P-35,382  
 REFERENCE/DOCKET NUMBER: 18685  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-3904  
 TELEFAX: (908) 594-4720  
 SEQUENCE FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 465 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-482-971-1

Query Match 92.1%; Score 105; DB 3; Length 465;  
 Best Local Similarity 87.0%; Pred. No. 3.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAFAASMAAFNTVNF 23  
 | | | | | | | : | | | | | | | : | | |  
 Db 121 NYFLVNLAFAASMAAFNTVNF 143

RESULT 11  
 US-09-826-509-529  
 / Sequence 529, Application US/09826509  
 / Patent No. 6806054  
 / GENERAL INFORMATION:  
 / APPLICANT: Lehmann-Bruinsma, Karin  
 / APPLICANT: Liaw, Chen W.  
 / APPLICANT: Lin, I-Lin  
 / TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G  
 / TITLE OF INVENTION: Protein-Coupled Receptors  
 / FILE REFERENCE: AREN-207  
 / CURRENT APPLICATION NUMBER: US/09/826,509  
 / CURRENT FILING DATE: 2001-04-05  
 / PRIOR APPLICATION NUMBER: 60/195,747  
 / PRIOR FILING DATE: 2000-04-07  
 / PRIOR APPLICATION NUMBER: 09/170,496  
 / PRIOR FILING DATE: 1998-10-13  
 / NUMBER OF SEQ ID NOS: 589  
 / SEQ ID NO: 529  
 / LENGTH: 465  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-09-826-509-529

Query Match 92.1%; Score 105; DB 4; Length 465;  
 Best Local Similarity 87.0%; Pred. No. 3.3e-08;  
 Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAFAASMAAFNTVNF 23  
 | | | | | | | : | | | | | | | : | | |  
 Db 121 NYFLVNLAFAASMAAFNTVNF 143

RESULT 12  
 US-08-390-000A-6  
 / Sequence 6, Application US/08390000A  
 / Patent No. 598583  
 / GENERAL INFORMATION:  
 / APPLICANT: Saitoff, Stuart C.  
 / TITLE OF INVENTION: Cloning and Expression of  
 / Gondotropin-Releasing Hormone Receptor  
 / NUMBER OF SEQUENCES: 8  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Pennie & Edmonds LLP  
 / STREET: 1135 Avenue of the Americas  
 / CITY: New York  
 / STATE: New York  
 / COUNTRY: U.S.A.  
 / ZIP: 10036-2711  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/390,000A  
 / FILING DATE: 17-FEB-1995  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Misrock, S. Leslie  
 / REGISTRATION NUMBER: 18,872  
 / REFERENCE/DOCKET NUMBER: 6923-052  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 212 790-9990  
 / TELEFAX: 212 863-8864/9741  
 / INFORMATION FOR SEQ ID NO: 6:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 407 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: unknown  
 / MOLECULE TYPE: protein  
 / US-08-390-000A-6

Query Match 91.2%; Score 104; DB 2; Length 407;  
 Best Local Similarity 91.3%; Pred. No. 4e-08;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYFLVNLAFAASMAAFNTVNF 23  
 | | | | | | | : | | | | | | | : | | |  
 Db 68 NYFLVNLAFAASMAAFNTVNF 90

RESULT 13  
 US-08-118-270-50  
 / Sequence 50, Application US/08118270  
 / Patent No. 550834  
 / GENERAL INFORMATION:  
 / APPLICANT: Murphy, Randall B.  
 / APPLICANT: Schuster, David I.  
 / TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
 / NUMBER OF SEQUENCES: 348  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: BROWDY AND NEIMARK  
 / STREET: 419 Seventh Street, N.W., Suite 300  
 / CITY: Washington  
 / STATE: D.C.  
 / COUNTRY: USA  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270  
 FILING DATE: 09-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/943,236  
 FILING DATE: 10-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Townsend, Kevin G.  
 REFERENCE DOCKET NUMBER: 34,033  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 50:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 336 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-118-270-50

Query Match 87.7%; Score 100; DB 1; Length 336;  
 Best Local Similarity 78.3%; Pred. No. 1.3e-07;  
 Matches 18; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAFAEASMAAFNTVNF 23  
 Db 37 NYFLVNLAFAEASMAAFNTVNF 59

RESULT 15  
 US-07-937-609-21  
 Sequence 21, Application US/07937609  
 ; Patent No. 5319073  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WANK, Stephen A.  
 ; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF  
 ; CHOECYSTOKININ RECEPTOR ENCODING DNA  
 ; NUMBER OF SEQUENCES: 29  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 1800 Diagonal Road, Suite 500  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0 Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/937,609  
 ; FILING DATE: 1992-09-02  
 ; CLASSIFICATION: 436  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/831,248  
 ; FILING DATE: 07-FEB-1992  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/861,769  
 ; FILING DATE: 01-APR-1992  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/928,033  
 ; FILING DATE: 11-AUG-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 40399/166 NIH  
 ; REFERENCE/DOCKET NUMBER: 40399/166 NIH  
 ; TELECOMMUNICATION:  
 ; TELEPHONE: (703) 836-9200  
 ; TELEFAX: (703) 683-4109  
 ; TELEX: 899149  
 ; INFORMATION FOR SEQ ID NO: 21:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 411 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; US-07-937-609-21

Query Match 87.7%; Score 100; DB 1; Length 411;  
 Best Local Similarity 78.3%; Pred. No. 1.7e-07;  
 Matches 18; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYFLVNLAFAEASMAAFNTVNF 23  
 Db 108 NYFLVNLAFAEASMAAFNTVNF 130

Search completed: April 19, 2005, 14:52:39  
 Job time : 48 secs

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OM protein - protein search, using sw model

Run on: April 19, 2005, 14:43:54 ; Search time 176 Seconds (without alignments)

66.919 Million cell updates/sec

Title: US-10-665-184-24

Perfect score: 114

Sequence: 1 NYFLVNLAFEAESMAAFNTVVNF 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100‡

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is greater by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	311	2 Q8R1R6	Q8r1r6 cavia porce
2	114	100.0	407	1 NK1R_CAVPO	P30547 cavia porce
3	114	100.0	407	1 NK1R_HUMAN	P25103 homo sapien
4	111	97.4	309	2 Q9DGJ9	Q9dgj9 bufo marinus
5	111	97.4	371	2 Q8O0X0	Q8o0x0 bufo marinus
6	111	97.4	390	2 QBJFP8	Qbjfp8 bufo marinus
7	111	97.4	411	2 Q9W6I3	Q9w6i3 gallus gallus
8	110	96.5	393	2 IPR01681	Q7t078 fugu rubripinnis
9	110	96.5	408	1 NK1R_RANCA	Q98982 rana catesbeiana
10	109	95.6	407	1 NK1R_MOUSE	P30548 mus musculus
11	109	95.6	407	1 NK1R_RAT	P14600 rattus norvegicus
12	109	95.6	407	2 QBYR7	Q8byr7 mus musculus
13	105	92.1	465	1 NK3R_HUMAN	P29371 homo sapien
14	105	92.1	467	1 NK3R_RABIT	P07552 oryctolagus cuniculus
15	101	88.6	452	1 NK3R_MOUSE	P47937 mus musculus
16	100	87.7	452	1 NK3R_RAT	P16177 rattus norvegicus
17	97	85.1	452	2 Q6NXX1	Q6nxx1 mus musculus
18	85	74.6	157	2 Q925R5	Q925r5 cavia porcellus
19	85	74.6	440	1 NK3R_CAVPO	P30098 cavia porcellus
20	79	69.3	130	2 Q96KE0	Q96ke0 homo sapien
21	79	69.3	384	1 NK2R_BOVIN	P05363 bos taurus
22	79	69.3	398	1 NK2R_HUMAN	P21522 homo sapien
23	79	69.3	398	2 Q8NGQ8	Q8ngq8 homo sapien
24	79	69.3	398	2 Q9UDE6	Q9ude6 homo sapien
25	79	69.3	402	1 NK2R_CAVPO	Q64077 cavia porcellus
26	78	68.4	384	1 NK2R_MESAU	P51144 mesocricetus auratus
27	78	68.4	384	1 NK2R_MOUSE	P30549 mus musculus
28	78	68.4	384	2 Q8BZV9	Q8bzv9 mus musculus
29	78	68.4	390	1 NK2R_RAT	P16610 rattus norvegicus
30	78	68.4	431	2 Q8T8D1	Q8t8d1 urechis unicinctus
31	75	65.8	384	1 NK2R_RABIT	P79218 oryctolagus cuniculus

RESULT 1

Q8R1R6 PRELIMINARY; PRT: 311 AA.

Q8R1R6; AC: DT: 01-JUN-2002 (TREMBLrel. 21, Created) DT: 01-JUN-2002 (TREMBLrel. 21, Last sequence update) DT: 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DE: Truncated neurokinin-1 receptor.

OS: Cavia porcellus (Guinea pig). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia. NCBI\_TaxID:10141; [1]

RN: RP: SEQUENCE FROM N.A.

RC: STRAIN=Hartley IMVS; TISSUE=Celiac ganglion; MEDLINE=2254021; PubMed=12654513; DOI=10.1016/S0169-328X(03)00002-0; RA: Baker S.J., Morris J.L., Gibbons I.L.; RT: "Cloning of a C-terminally truncated NK-1 receptor from guinea-pig nervous system." RL: Brain Res. Mol. Brain Res. 111:135-147(2003).

CC: 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity). CC: 1- SIMILARITY: Belongs to Family 1 of G-protein coupled receptors.

EMBL: AF128266; AAU89641; -.

DR: DR: C integral to membrane; IEA.

DR: DR: GO:0016023; C integral to membrane; IEA.

DR: DR: GO:0005886; C plasma membrane; IEA.

DR: DR: GO:0004872; F: receptor activity; IEA.

DR: DR: GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR: DR: GO:0004995; F: tachykinin receptor activity; IEA.

DR: DR: GO:0007188; P: G-protein coupled receptor activity; IEA.

DR: DR: InterPro: IPR00276; GPR7 Rhodopsin.

DR: DR: InterPro: IPR01681; Neurokin receptor.

DR: DR: InterPro: IPR00044; NK1 receptor.

DR: DR: Pfam: PF00017tm\_1; 1.

DR: DR: PRINTS: PRO0237; GPCRHDOPSN.

DR: DR: PRINTS: PRO1034; NEUROKININR.

DR: DR: PROSITE: PS00237; G PROTEIN RECEP\_F1\_1; 1.

DR: DR: PROSITE: PS00237; G PROTEIN RECEP\_F1\_2; 1.

KW: G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE: 315702 MW; 311 AA;

Query Match: Score 114; DB 2; Length 311; Best Local Similarity 100.0%; Pred. No. 1.7e-09; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy: 1 NYFLVNLAFEAESMAAFNTVVNF 33  
68 NYFLVNLAFEAESMAAFNTVVNF 90

Db: AC: P30547;

RESULT 2

NK1R\_CAVPO ID: NK1R\_CAVPO STANDARD; PRT: 407 AA.





DR	GO:0001584; F: rhodopsin-like receptor activity; IEA.	DT	01-NOV-1999 (TREMBLrel. 12, Created)
DR	GO:0001585; F: tachykinin receptor activity; IEA.	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DR	GO:0007186; G:G-protein coupled receptor protein signalin.. . ; IEA.	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DR	InterPro; IPR000216; GPCR Rhodpsn.	DE	Substance P receptor.
DR	InterPro; IPR001681; Neurokin receptor.	GN	Name=ASPR;
DR	PFam; PF00001; 7tm_1..1.	OS	Galus gallus (Chicken)
DR	PRINTS; PR00237; GPCRRRHODOPSN.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
DR	PRINTS; PS00237; G:PROTEIN RECEP_F1_1..1.	OC	NCBI_TaxID:9031;
DR	PROSITE; PS52622; G:PROTEIN RECEP_F1_2..1.	OX	[1]_RN
DR	PROSITE; PS52623; G:PROTEIN RECEP_F1_1..1.	RP	SEQUENCE FROM N.A.
KW	G-protein coupled receptor; Receptor; Transmembrane.	RC	TISSUE=Brain;
SQ	SEQUENCE 371 AA; 43094 MW; 59A063A271A75B9 CRC64;	RA	Sia G.M., Maggio J.E., Too H.P.; Submitted (PRB-1999) to the EMBL/GenBank/DBJ databases
		RL	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
		CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
		CC	-1- SIMILARITY: AAD31017.1; -.
		DR	GO; GO:0016212; C:integral to membrane; IEA.
		DR	GO; GO:0005886; C:plasma membrane; IEA.
		DR	GO; GO:0009872; F:receptor activity; IEA.
		DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
		DR	InterPro; IPR000216; GPCR_Rhodpsn.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
SQ	SEQUENCE 411 AA; 47090 MW; 3528DB96A046159 CRC64;	SEQUENCE	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	411 AA; 47090 MW; 3528DB96A046159 CRC64;
		RESULT 8	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	72 NYFLVNLAFAEAMAFNTVNF 94	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 9	
		Query Match	97.4%; Score 111; DB 2; Length 390;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 7	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 8	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 9	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 10	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 11	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 12	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 13	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 14	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 15	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 16	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db	67 NYFLVNLAFAEAMAFNTVNF 89	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_2..1.
		DR	InterPro; IPR000046; NK1 receptor.
		DR	InterPro; IPR001681; Neurokin receptor.
		DR	InterPro; PR00001; 7tm_1..1.
		DR	PRINTS; PR00237; GPCRRRHODOPSN.
		DR	PRINTS; PR01024; NEUROKININR.
		DR	PRINTS; PR00244; NEUROKININR.
		DR	PROSITE; PS00237; G:PROTEIN RECEP_F1_1..1.
		DR	PROSITE; PS500262; G:PROTEIN RECEP_F1_2..1.
		KW	G-protein coupled receptor; Receptor; Transmembrane.
		SEQUENCE	390 AA; 45091 MW; ACB6B77B9A88671 CRC64;
		RESULT 17	
		Query Match	97.4%; Score 111; DB 2; Length 411;
		Best Local Similarity	95.7%; Pred. No. 6..e-09; DB 2/
		Matches	22; Conservative 1; Mismatches 0; Gaps 0; Gaps 0;
Qy	1 NYFLVNLAFAEAMAFNTVNF 23	DR	InterPro; IPR000216; G:PROTEIN RECEP_F1_1..1.
Db</			

DR	PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.	FT	TRANSMEM	197	221	5 (Potential).
KW	G-protein coupled receptor; Transmembrane.	FT	TRANSMEM	222	250	Cytoplasmic (Potential).
SQ	SEQUENCE 393 AA; 45114 MW; 7F508031ADFD57F8 CRC64;	FT	TRANSMEM	251	272	6 (Potential).
	Query Match 96.5%; Score 110; DB 2; Length 393; Best Local Similarity 91.3%; Pred. No. 9.1e-09; Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Sq	FT	TRANSMEM	273	283	Extracellular (Potential).
Qy	1 NYFLVNLAFAEASMAAFNTVNF 23	FT	TRANSMEM	284	308	7 (Potential).
Db	72 NYFLVNLAFAEASMSAFNTVNF 94	FT	CARBHYD	309	408	Cytoplasmic (Potential).
		FT	CARBHYD	4	4	N-linked (GlcNAc. . .) (Potential).
		FT	CARBHYD	9	9	N-linked (GlcNAc. . .) (Potential).
		FT	CARBHYD	14	14	N-linked (GlcNAc. . .) (Potential).
		FT	CARBHYD	19	19	By similarity.
		FT	DISULPID	106	181	S-palmitoyl cysteine (Potential).
		FT	LIPID	323	323	S-palmitoyl cysteine (Potential).
		SQ	SEQUENCE	408 AA;	47010 MW;	300C28AEB820240E CRC64;
RESULT 9						
ID	NK1_RANCA	STANDARD;	PRY;	408 AA.		Query Match 96.5%; Score 110; DB 1; Length 408; Best Local Similarity 91.3%; Pred. No. 9.5e-09; Mismatches 2; Indels 0; Gaps 0;
AC	Q98982;					
DT	01-NOV-1997 (Rel. 35, Created)					
DT	01-NOV-1997 (Rel. 35, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Substance-P receptor (SPR) (NK-1 receptor) (DE receptor 1).					
GN	Name=TACR1; Synonyms=TACR1;					
OS	Rana catesbeiana (Bull Frog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.					
OC	NCBI_TaxID=8400;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	SEQUENCE FROM N.A.					
RC	TISSUE=Sympathetic ganglion; PubMed=9219980; DOI=10.1016/S0306-4522(97)00027-4;					
RC	LINEID=97363687; PubMed=9219980; DOI=10.1016/S0306-4522(97)00027-4;					
RA	Simmons M.A., Brodbeck R.M., Karpluski V.V., Schneider C.R., Neff D.P.A., Krause J.E., RT					
RA	"Molecular characterization and functional expression of a substance P receptor from the sympathetic ganglion of Rana catesbeiana.",					
RA	Neuroscience 79:1219-1229(1997).					
RL	-1- FUNCTION: This is a receptor for the tachykinin neuropeptide substance P. It is probably associated with G proteins that activate a phosphatidylinositol-calcium second messenger system.					
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.					
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage "by" and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch">http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch</a> ).					
CC	-----					
CC	CC -1- This is a receptor for the tachykinin neuropeptide substance P. It is probably associated with G proteins that activate a phosphatidylinositol-calcium second messenger system.					
CC	CC -1- SUBCELLULAR LOCATION: Integral membrane protein.					
CC	CC -1- MISCELLANEOUS: The rank order of affinity of this receptor to tachykinins is: substance P > substance K > neuropeptide K receptor ".					
CC	CC -1- FUNCTION: This is a receptor for the tachykinin neuropeptide substance P. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage "by" and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch">http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch</a> ).					
CC	CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.					
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage "by" and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch">http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch</a> ).					
DR	HSSP; P02699; 1F8B.	FT	TRANSMEM	32	Extracellular (Potential).	
DR	IntersPro; IPR001276; GPCR_Rhodopsin.	FT	TRANSMEM	33	1 (Potential).	
DR	IntersPro; IPR001681; Neurokin receptor.	FT	TRANSMEM	56	Cytoplasmic (Potential).	
DR	Prosite; PS00237; G-PROTEIN RECEP_F1_1; 1.	FT	TRANSMEM	66	2 (Potential).	
KW	G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation; Transmembrane.	FT	TRANSMEM	88	Extracellular (Potential).	
FT	TRANSMEM	FT	TRANSMEM	108	3 (Potential).	
FT	TRANSMEM	FT	TRANSMEM	130	Cytoplasmic (Potential).	
FT	TRANSMEM	FT	TRANSMEM	150	4 (Potential).	
FT	TRANSMEM	FT	TRANSMEM	196	Extracellular (Potential).	

DR	EMBL; L27828; AAA17892;1; -.	receptor.";
DR	EMBL; L27826; AAA17891;1; -.	J. Biol. Chem. 264:17649-17652 (1989).
DR	S20304; S20304.	RN [3]
DR	MGD; MGI:98415; Tacrl.	RN
DR	GO: GO:0048265; P: response to pain; IMP.	RP
DR	InterPro; IPR0027; GPCR_Rhodopsin.	SEQUENCE FROM N.A.
DR	InterPro; IPR001681; Neurokinin receptor.	STRAIN-Sprague-Dawley;
DR	InterPro; IPR000446; NK1_receptor.	MEDLINE=90161991; PubMed=2154852;
DR	Prints; PRO0001; Tcr1; 1.	Hershey A.D.; Krause J.E.;
DR	Prints; PRO004; NEUROKININ1R.	"Molecular characterization of a functional cDNA encoding the rat substance P receptor."
DR	Prints; PRO0237; GPCR_RHODOPSN.	substance P receptor.";
DR	Prints; PRO0024; NEUROKININ1R.	Science 247:958-962 (1990).
DR	Prints; PRO00237; G_PROTEIN_RECCEP_F1; 1.	[4]
DR	Prints; PRO00237; G_PROTEIN_RECCEP_F1; 2; 1.	RN
DR	Prints; PRO00237; G_protein_recceptor; Glycoprotein; Lipoprotein; Palmitate; KW G-protein coupled receptor; Transmembrane.	RN
DR	Prints; PRO00237; G_protein_recceptor; Glycoprotein; Lipoprotein; Palmitate; KW G-protein coupled receptor; Transmembrane.	RN
FT	DOMAIN 1 31 54 Extracellular (Potential).	RA Hershey A.D.;
FT	DOMAIN 1 31 54 Extracellular (Potential).	RA Submitted (PEB-1996) to the EMBL/GenBank/DBJ databases.
FT	TRANSMEM 32 54 Extracellular (Potential).	RN [3]
FT	DOMAIN 55 64 Cytoplasmic (Potential).	CC
FT	TRANSMEM 65 86 Extracellular (Potential).	CC
FT	DOMAIN 87 106 Extracellular (Potential).	CC
FT	TRANSMEM 107 128 3 (Potential).	CC
FT	DOMAIN 129 148 Cytoplasmic (Potential).	CC
FT	TRANSMEM 149 169 4 (Potential).	CC
FT	DOMAIN 170 194 Extracellular (Potential).	CC
FT	TRANSMEM 195 219 5 (Potential).	CC
FT	DOMAIN 220 248 6 (Potential).	CC
FT	TRANSMEM 249 270 7 (Potential).	CC
FT	DOMAIN 271 283 Extracellular (Potential).	CC
FT	TRANSMEM 284 308 7 (Potential).	CC
FT	DOMAIN 309 407 Cyctoplasmic (Potential).	CC
FT	CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).	CC
FT	CARBOHYD 18 18 N-linked (GlcNAc. . .) (Potential).	CC
FT	DISULFID 105 180 By similarity.	CC
FT	LIPID 322 322 S-palmitoyl cysteine (Potential).	CC
SQ	SEQUENCE 407 AA; 46304 MW; 451B6D475A6659A0 CRC64;	CC
Query Match	95.6%; Score 109; DB 1; Length 407;	CC
Best Local Similarity	95.7%; Pred. No. 1.4e-08; Gaps 0;	CC
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	CC	
YQ	1 NYFLVNLAPEAASMAAFNTVNF 23	PRINTS; PRO00237; GPCR_RHODOPSN.
Db	68 NYFLVNLAPEAASMAAFNTVNF 90	PRINTS; PRO00237; GPCR_RHODOPSN.
YQ	1 NYFLVNLAPEAASMAAFNTVNF 23	PRINTS; PRO00244; NEUROKININ1R.
Db	68 NYFLVNLAPEAASMAAFNTVNF 90	PRINTS; PRO00244; NEUROKININ1R.
RESULT 11		DR InterPro; IPR000276; GPCR_Rhodopsin.
NRK_RAT	STANDARD;	DR InterPro; IPR001681; Neurokinin receptor.
ID_NK1_RAT	PRT; 407 AA.	DR InterPro; IPR000446; NK1_receptor.
AC		DR PROSITE; PS00237; G-PROTEIN_RECCEP_F1; 1.
PI4600;		DR PROSITE; PS00562; G-PROTEIN_RECCEP_F1; 2.
DR	01-APR-1990 (Rel. 14, Created)	KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
DR	01-APR-1990 (Rel. 14, Last sequence update)	FT DOMAIN 1 31 Extracellular (Potential).
DE	25-OCT-2004 (Rel. 45, Last annotation update)	FT TRANSMEM 32 54 Cytoplasmic (Potential).
DB	Substance-P receptor (SPR) (NK-1 receptor) (NK-1R) (Tachykinin receptor 1).	FT TRANSMEM 55 64 2 (Potential).
RN		FT TRANSMEM 65 86 Extracellular (Potential).
[1]		FT TRANSMEM 87 106 5 (Potential).
OS	Rattus norvegicus (Rat).	FT TRANSMEM 107 128 3 (Potential).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	FT TRANSMEM 129 148 Cytoplasmic (Potential).
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	FT TRANSMEM 149 169 4 (Potential).
NCBI_TaxID=10116;		FT TRANSMEM 170 194 Extracellular (Potential).
RN		FT TRANSMEM 195 219 5 (Potential).
[1]		FT TRANSMEM 220 248 Cytoplasmic (Potential).
RP	SEQUENCE FROM N.A.	FT TRANSMEM 249 270 6 (Potential).
RP	MEDLINE=91154239; PubMed=1705552;	FT DOMAIN 271 283 Extracellular (Potential).
RA	Hershey A.D.; Dykema P.B.; Krause J.E.;	FT TRANSMEM 284 308 7 (Potential).
RT	"Organization, structure, and expression of the gene encoding the rat substance P receptor."	FT TRANSMEM 309 407 Cytoplasmic (Potential).
RT	J. Biol. Chem. 266:4366-4374 (1991).	FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
[2]		FT CARBOHYD 15 18 N-linked (GlcNAc. . .) (Potential).
RP	SEQUENCE FROM N.A.	FT DISULFID 105 180 By similarity.
RX	MEDLINE=90036822; PubMed=2478537;	FT LIPID 322 322 S-palmitoyl cysteine (Potential).
RA	Sasaki Y., Tanaka K., Fujiwara T., Tsuchida K.,	FT CONFLICT 73 73 N (In Ref. 3).
RA	Shigemoto R., Kakizuka A., Ohkubo H., Nakaniishi S.;	RA MEDF05A0BF551C96 CRC64;
RT	"Molecular characterization of a functional cDNA for rat substance P	RT

Query Match	95.6%	Score 109; DB 1; Length 407;	RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirozane T., Kaga T., Kondo M., Kaga T., Kondo M., Koya S., Kotoh H., Kawai J., Kojima Y., Kondo S., Kondo H., Kondo M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takagawa Y., Takeda Y., Tomita T., Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Best Local Similarity	95.7%	Score 104; DB 0; Length 408;	RA	Hori F., Imotani K., Ishii Y., Itoh M., Kaga T., Kondo M., Kaga T., Kondo M., Koya S., Kotoh H., Kawai J., Kojima Y., Kondo S., Kondo H., Kondo M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takagawa Y., Takeda Y., Tomita T., Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Matches 22;	Conservative 0;	DBI matches 1; Indels 0; Gaps 0;	RA	Hori F., Imotani K., Ishii Y., Itoh M., Kaga T., Kondo M., Kaga T., Kondo M., Koya S., Kotoh H., Kawai J., Kojima Y., Kondo S., Kondo H., Kondo M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takagawa Y., Takeda Y., Tomita T., Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Db	1 NYFLVNLAFAEASMAAFNTVNF 23 68 NYFLVNLAFAEACMAAFNTVNF 90		RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RESULT 12			RN	[17]
QBYR7	PRELIMINARY;	PRT;	RP	SEQUENCE FROM N.A.
ID	QBYR7		RC	STRAIN=CS7BL/6; TISSUE=Brain;
DT	08BY7;		RX	MEDLINE=2388237; PubMed=12477932; DOI=10.1073/pnas.242603899;
DT	01-MAR-2003 (T-EMBLrel. 23; Created)		RA	Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schulz G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheuer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schuetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Garniuci P., Prange C., Raha S.S., Logueillan A.A., Peters G.J., Abramson R.D., Mullhy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.J., Skalska U., Smalius D.E., Schnarch A., Schein J.E., Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; R.L. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[1]		RA	[18]
RP	SEQUENCE FROM N.A.		RP	SEQUENCE FROM N.A.
RC	STRAIN=CS7BL/6; TISSUE=Hypothalamus;		RC	STRAIN=CS7BL/6; TISSUE=Brain;
RX	MEDLINE=99279253; PubMed=101650076-6879 (99)03004-9;		RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA	Carninci P., Hayashizaki Y.;		CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
RT	"High-efficiency full-length cDNA cloning.";		CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
RT	Meth. Enzymol. 303:19-44(1999).		DR	AK038558; BAC30042.1; -.
RN	[2]		DR	EMBL; BC075632; AAH75631.1; -.
RP	SEQUENCE FROM N.A.		DR	MGI: MG1-98475; Tacr1.
RC	STRAIN=CS7BL/6J; TISSUE=Hypothalamus;		DR	GO; GO:0016021; C: integral to membrane; TAS
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;		DR	GO; GO:0048265; P: response to pain; IMP.
RA	"Functional annotation of a full-length mouse cDNA collection.";		DR	InterPro; IPR00276; GPCR_Rhodopsin.
RT	"Functional annotation of a full-length mouse cDNA collection.";		DR	InterPro; IPR00046; NeuRokin receptor.
RN	Nature 409:685-690 (2001).		DR	PRINTS; PR00237; PS000237; G PROTEIN RECEP_F1_1.
RN	[3]		DR	PROSITE; PS50062; G PROTEIN RECEP_F1_2; 1.
RP	SEQUENCE FROM N.A.		KW	G-protein coupled receptor; Receptor; Transmembrane.
RC	STRAIN=CS7BL/6J; TISSUE=Hypothalamus;		SEQUENCE	407 AA; 46331 MW; 451B6B875A6659A0 CRC64;
RA	THE FANTOM Consortium,		Query Match	95.6%; Score 109; DB 2; Length 407;
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		Best Local Similarity	95.7%; Pred. No. 1.4e-08;
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";		Matches	22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RT	Nature 420:563-573 (2002).		Qy	1 NYFLVNLAFAEASMAAFNTVNF 23 68 NYFLVNLAFAEACMAAFNTVNF 90
RN	[4]		Db	RESULT 13
RP	SEQUENCE FROM N.A.		NK3R_HUMAN	
RC	STRAIN=CS7BL/6J; TISSUE=Hypothalamus;		ID	NK3R_HUMAN
RA	MEDLINE=20499374; PubMed=1102159; DOI=10.1101/gr.145100;		AC	P2971;
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kondo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;		DT	01-DBC-1992 (Rel. 24, Created)
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";			
RT	Genome Res. 10:1617-1630 (2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CS7BL/6J; TISSUE=Hypothalamus;			
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishimi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishihira T., Hayada A., Yamamoto R., Matsuboto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;			
RT	"RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer.";			
RT	Genome Res. 10:1757-1771 (2000).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CS7BL/6J; TISSUE=Hypothalamus;			
RA	SEQUENCE FROM N.A.			
RA	STRAIN=CS7BL/6J; TISSUE=Hypothalamus;			
RA	AC			
RA	Db			

01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DR Neurokinin K receptor (NKR) (Neurokinin B receptor) (NK-3 receptor)  
 DE (NR-3R) (Tachykinin receptor 3).  
 DE Name=TACR3; Synonyms=NKR3R, TAC3R;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=92246993; PubMed=1374246;  
 RT "cDNA sequence and heterologous expression of the human neurokinin 3 receptor.";  
 RT Biochem. Biophys. Res. Commun. 184: 966-972 (1992).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=92133914; PubMed=1312036; DOI=10.1016/0014-5793(92)80107-R;  
 RX Buell G., Schulz, M.F., Arkinstall, S.J., Maury K., Missotten M.,  
 RA Adami N., Talabot F., Kawashima E.;  
 RT "Molecular characterisation, expression and localisation of human neurokinin-3 receptor";  
 RT FEBS Lett. 299:90-95 (1992).  
 [3]  
 SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=92201186; PubMed=1312928;  
 RA Takahashi K., Tanaka A., Hara M., Nakanishi S.;  
 RT "the primary structure and gene organization of human substance P and neurokinin K receptors";  
 RJ Eur. J. Biochem. 204:1025-1033 (1992).  
 CC -!- FUNCTION: This is a receptor for the tachykinin neuropeptide neurokinin K (neurokinin B). It is associated with G proteins that activate a phosphatidylinositol-calcium second messenger system.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- PTM: The anchoring of this receptor to the plasma membrane is probably mediated by the palmitoylation of a cysteine residue.  
 CC -!- MISCELLANEOUS: The rank order of affinity of this receptor to tachykinins ie: neurokinin K > substance K > substance P.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC DR EMBL; S66392; AAB1706.1; -.  
 DR EMBL; S66371; AAB1706.1; JOINED.  
 DR EMBL; S66382; AAB21706.1; JOINED.  
 DR EMBL; S66388; AAB21706.1; JOINED.  
 DR EMBL; S66390; AAB21706.1; JOINED.  
 DR EMBL; S66392; AAA16366.1; -.  
 DR EMBL; X55172; CAA46291.1; -.  
 DR EMBL; X55173; CAA46291.1; JOINED.  
 DR EMBL; X55174; CAA46291.1; JOINED.  
 DR EMBL; X55175; CAA46291.1; JOINED.  
 DR EMBL; X55176; CAA46291.1; JOINED.  
 DR PIR; JO1517; JO1517.  
 DR HSSP; P22699; 1P88; TACR3.  
 DR Genew; IP2332; -.  
 DR MIM: 162332; -.  
 DR GO; GO:0005887; C integral to plasma membrane; TAS.  
 DR GO; GO:0004935; Tachykinin receptor activity; TAS.  
 DR GO; GO:0007237; Tachykinin signaling pathway; TAS.  
 DR InterPro; IPR000226; GPCR\_Rhodopsin.  
 DR InterPro; IPR001631; Neurokinin receptor.  
 DR InterPro; IPR001033; NK3 receptor.  
 DR Pfam; PF00001; 7m1\_1.

CC DR PRINTS; PRO0237; GPCR\_RHODOPSN.  
 DR PRINTS; PRO1026; NEUROKININ3R.  
 DR PRINTS; PRO0244; NEUROKININR.  
 DR PROSITE; PS01023; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS050262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation; Transmembrane.  
 KW DOMAIN 1 84  
 FT TRANSMEM 1 84  
 FT DOMAIN 1 107  
 DR DOMAIN 108 117  
 DR TRANSMEM 118 139  
 FT DOMAIN 140 159  
 FT TRANSMEM 160 181  
 FT DOMAIN 182 201  
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 FT DOMAIN 360 465  
 DR DOMAIN 465 5  
 DR DISULFID 158 233  
 DR LIPID 374 374  
 DR CARBOHYD 23 23  
 DR CARBOHYD 50 50  
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 DR CONFLICT 3 3  
 DR CONFLICT 63 63  
 DR CONFLICT 439 439  
 SQ SEQUENCE 465 AA; 52201 MW; 98BB8D4BC9DBD315 CRC64;

Query March 2005: Score 105; DB: 1; Length: 465;  
 Best Local Similarity: 87.0%; Pred. No. 6.6e-08;  
 Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYPLVNLAFASMAAFTVNF 23  
 Db 121 NYPLVNLAFASMAAFTVNF 143

RESULT 14  
 NK3\_RABBIT  
 ID NCBI\_RABBIT  
 AC O97512;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2004 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Neurokinin K receptor (NKR) (Neurokinin B receptor) (NK-3 receptor)  
 DE (NK-3R) (Tachykinin receptor 3).  
 GN Name=TACR3;  
 RN Sequence from N.A.  
 RN ID NCBI\_RABBIT  
 RN STANDARD;  
 RN PRT; 467 AA.  
 OC Mammalia; Buthidae; Lagomorpha; Leporidae; Oryctolagidae;  
 OC Oryctolagus cuniculus (Rabbit);  
 OC Striatus; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Buthidae; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Buthidae; Lagomorpha; Leporidae; Oryctolagidae;  
 OC OX NCBI\_TaxID=9986;  
 RN PRT muscle;";  
 RC RBL; J. Pharmacol. 128:627-636 (1999).  
 RC MEDLINE=9947488; PubMed=10516642;  
 RX RA Medhurst A.D., Hirst W.D., Jerman J.C., Meakin J., Roberts J.C.,  
 RA Testa T., Smart D.;  
 RA "Molecular and pharmacological characterization of a functional tachykinin NK3 receptor cloned from the rabbit iris sphincter muscle".  
 CC -!- FUNCTION: This is a receptor for the tachykinin neuropeptide neurokinin K (neurokinin B). It is associated with G proteins that activate a phosphatidylinositol-calcium second messenger system  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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InterPro; IPR001013; NR3_receptor.
DR Pfam; PR00001; 7cm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01026; NEUROKININ1R.
DR PRINTS; PR00244; NEUROKININ1R.
DR PROSITE; PS00037; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECCEP_F1_2; 1.
DR G_protein_coupled_receptor; Glycoprotein; Lipoprotein; Palmitate;
KW phosphorylation; Transmembrane.
FT DOMAIN 1 71 Extracellular (Potential).
FT TRANSMEM 72 94 1 (Potential).
FT DOMAIN 95 104 Cycloplasmic (Potential).
FT TRANSMEM 105 126 2 (Potential).
FT DOMAIN 127 146 Extracellular (Potential).
FT TRANSMEM 147 168 3 (Potential).
FT DOMAIN 169 188 Cycloplasmic (Potential).
FT TRANSMEM 189 209 4 (Potential).
FT DOMAIN 210 232 Extracellular (Potential).
FT TRANSMEM 233 257 5 (Potential).
FT DOMAIN 258 286 Cycloplasmic (Potential).
FT TRANSMEM 287 308 6 (Potential).
FT DOMAIN 309 321 Extracellular (Potential).
FT TRANSMEM 322 346 7 (Potential).
FT DOMAIN 347 452 Cycloplasmic (Potential).
* FT CARBOHYD 9 9 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 23 23 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 40 40 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 60 60 N-linked (GlcNAc. .) (Potential).
FT DISULFID 145 220 N-linked (GlcNAc. .) (Potential).
FT LIPID 361 361 S-palmitoyl cysteine (Potential).
FT CONFLICT 59 59 A -> D (in Ref. 3).
FT CONFLICT 198 198 A -> S (in Ref. 4).
FT CONFLICT 267 267 P -> I (in Ref. 3).
FT CONFLICT 385 385 S -> P (in Ref. 3).
SQ SEQUENCE 452 AA; 51026 MW; 7A46D400AD7FC444 CRC64;

Query Match 88.6%; Score 101; DB 1; Length 452;
Best Local Similarity 82.6%; Pred. No. 2 7e-07;
Matches 19; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NYFLVNLLPAEASMAAFNTVNF 23
Db 108 NYFLVNLLPAEASMAAFNTVNF 130

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Search completed: April 19, 2005, 14:51:07  
 Job time : 188 secs

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	rhodopsin - giant opsin, Pinna glan
OM protein - protein search, using sw model		5-HT4S receptor - serotonin 4 receptor
Run on:	April 19, 2005, 14:43:54 ; Search time 43 Seconds (without alignments)	alpha-1-adrenergic receptor
	51.465 Million cell updates/sec	alpha-1B-adrenergic receptor
Title:	US-10-665-184-24	alpha-1B-adrenergic receptor
Perfect score:	114	alpha-1B-adrenergic receptor
Sequence:	1 NYFLVNLAFAEASMAAFNTVVF 23	protein TM3J18-28
Scoring table:	BLOSUM62	opsin, blue-sensit
	Gapop 10.0 , Gapext 0.5	cone visual pigment
Searched:	283416 seqs, 96216763 residues	uncharacterized co
Total number of hits satisfying chosen parameters:	283416	
Minimum DB seq length: 0		RESULT 1
Maximum DB seq length: 2000000000		JQ1274
Post-processing: Minimum Match 0 <sup>+</sup>		neurokinin 1 receptor - human
Maximum Match 100 <sup>+</sup>		N;Alternate names: NK-1 receptor; substance P receptor
Listing First 45 summaries		C;Species: Homo sapiens (man)
Database :	PIR 79:*	C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 09-Jul-2004
	1: pir1:*	C;Accession: A41134; JH0478; S21188
	2: pir2:*	R;Gerard, N.P.; Garrow, L.A.; Eddy, Jr., R.L.; Shows, T.B.; Iijima, H.; Paquet, J.L.; G
	3: pir3:*	Biochemistry 30, 10440-10446, 1991
	4: pir4:*	A;Title: Human substance P receptor (NK-1): organization of the gene, chromosome localiz
		A;Reference number: A41134; MUID:92031510; PMID:1657150
		A;Accession: A41134
		A;Molecule type: DNA
		A;Residues: 1-328,'G',129-332,334-407,<GER>
		A;Cross-references: UNIPROT:25103; GB:M76675; NID:gi189231
		A;Note: In the authors' translation, 331-Gly is shown before residue 329 and, consequent
		R;Takeeda, Y.; Chou, K.B.; Takenaka, J.; Sachais, B.S.; Krause, J.E.
		Biochem. Biophys. Res. Commun. 179, 122-124, 1991
		A;Title: Molecular cloning, structural characterization and functional expression of the
		A;Reference number: JQ1274; MUID:92028856; PMID:1718267
		A;Accession: JQ1274
		A;Molecule type: mRNA
		A;Residues: 1-407 <TAK1>
		A;Cross-references: GB:W74290; PIDN:AAA60601.1; PID:gi330613
		A;Experimental source: Lung
		A;Hopkins, B.; Powell, S.J.; Danko, P.; Brigham, A.
		Biochem. Biophys. Res. Commun. 180, 1110-1117, 1991
		A;Title: Isolation and characterization of the human lung NK-1 receptor cDNA.
		A;Reference number: JH0478; MUID:92062052; PMID:1659396
		A;Accession: JH0478
		A;Molecule type: mRNA
		A;Residues: 1-407 <HOP>
		A;Cross-references: GB:S62045; PID:gi237994; PIDN:AB20168.1; PID:g237995
		A;Experimental source: Lung
		A;The authors translated the codon CAA for residue 31 as Glu
		R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.
		Eur. J. Biochem. 204, 1025-1033, 1992
		A;Title: The primary structure and gene organization of human substance P and neuromedin
		A;Reference number: S21188; MUID:92201186; PMID:1312938
		A;Accession: S21188
		A;Status: Preliminary
		A;Molecule type: DNA
		A;Residues: 1-407 <TAK2>
		A;Cross-references: GB:X65177; NID:gi3636; PIDN:CAA46292.1; PID:g9825721
		C;Comment: The endogenous ligand of this receptor is neurokinin 1 (substance P), one of
		C;Genetics:
		A;Gene: TAC1R
		A;Cross-references: GDB:128977; OMIM:162323
		A;Map position: 2pter-2qter
		C;Superfamily: neurokinin 1 receptor
		C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein
		F;32-58/Domain: transmembrane #status predicted <TM1>
		F;69-92/Domain: transmembrane #status predicted <TM2>

A;Molecule type: mRNA  
A;Residues: 63-290 <C001>  
A;Cross-references: GB:127826; NID:9450286; PIDN:AAA17891.1; PMID:g480778  
A;Experimental source: tissue 'brain'  
A;Accession: 173044  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 63-290 <C002>  
A;Cross-references: GB:127828; NID:9450290; PIDN:AAA17892.1; PMID:g480778  
A;Experimental source: tissue 'granuloma'  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 95.6%; Score 109; DB 2; Length 407;  
Best Local Similarity 95.7%; Pred. No. 5.6e-10;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 NYFLVNLAFAASMAAFTNTVNF 23  
Db 68 NYFLVNLAFAEACMAAFTNTVNF 90

RESULT 4  
A34357  
neurokinin 1 receptor - rat  
N;Alternate names: NK-1 receptor; substance P receptor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2000  
C;Accession: A38692; A34357; A40089  
R;Hershey, A.D.; Dykema, P.E.; Krause, J.E.  
J. Biol. Chem. 266, 4366-4374, 1991  
A;Title: Organization, structure, and expression of the gene encoding the  
A;Reference number: A38852; MUID:91154239; PMID:1705552  
A;Accession: A38692  
A;Molecule type: DNA  
A;Residues: 1-407 <HR>  
A;Cross-references: UNIPROT:PI4600; GB:34751  
R;Yokota, Y.; Sasai, Y.; Tanaka, K.; Fujiwara, T.; Tsuchida, K.; Shigemoto, R.; Hershey, A.D.; Krause, J.E.  
J. Biol. Chem. 264, 17649-17652, 1989  
A;Title: Molecular characterization of a functional cDNA for rat substance P receptor  
A;Reference number: A34357; MUID:90036822; PMID:2478537  
A;Accession: A34357  
A;Molecule type: mRNA  
A;Residues: 1-407 <YOK>  
A;Cross-references: GB:J05097; NID:9207051; PIDN:AAA42175.1; PMID:g207052  
R;Hershey, A.D.; Krause, J.E.  
Science 247, 958-962, 1990  
A;Title: Molecular characterization of a functional cDNA encoding the rat substance P receptor  
A;Reference number: A40089; MUID:90161991; PMID:21344852  
A;Accession: A40089  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-74, 'R76-212,'A',214-407 <HE2>  
A;Cross-references: GB:W11477  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 95.6%; Score 109; DB 2; Length 407;  
Best Local Similarity 95.7%; Pred. No. 5.6e-10;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 NYFLVNLAFAASMAAFTNTVNF 23  
Db 68 NYFLVNLAFAEACMAAFTNTVNF 90

R;Huang, R.R.C.; Cheung, A.H.; Mazina, K.E.; Strader, C.D.; Fong, T.M.   
 Biochem. Biophys. Res. Commun. 184, 966-972, 1992   
 A;Title: cDNA sequence and heterologous expression of the human neurokinin-3 receptor.   
 A;Reference number: JQ1517; MUID:924693; PMID:1374246   
 A;Status: nucleic acid sequence not shown   
 A;Molecule type: mRNA   
 A;Residues: 1-65 <HUA>   
 A;Cross-references: UNIPROT:P29371; GB:M89473; PIDN:AAA3636.1; PMID:9189224   
 R;Busil, G.; Schulz, M.P.; Arkinstall, S.J.; Maury, K.; Missotten, M.; Adami, N.; Talaboc   
 PEBs Lett. 299, 90-95, 1992   
 A;Title: Molecular characterisation, expression and localisation of human neurokinin-3   
 A;Reference number: S20435; MUID:92183914; PMID:1312036   
 A;Accession: S20435   
 A;Status: preliminary   
 A;Molecule type: DNA   
 A;Residues: 1-62, 'R', 64-465 <BUE>   
 A;Cross-references: GB:SS6392; NID:9246908; PIDN:AAB21706.1; PMID:g246909   
 R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakaniishi, S.   
 Eur. J. Biochem. 204, 1055-1053, 1992   
 A;Title: The primary structure and gene organization of human substance P and neuropeptides   
 A;Reference number: S21188; MUID:92201186; PMID:1312928   
 A;Accession: S21237   
 A;Status: preliminary   
 A;Molecule type: DNA   
 A;Residues: 1-438, F', 440-465 <TAK>   
 A;Cross-references: GB:X55172; NID:935022; PIDN:CAA46221.1; PMID:g9825695   
 C;Comment: The endogenous ligand of this receptor is neurokinin 3 (neuropeptide K), one of   
 C;Genetics:   
 A;Gene: GDB:TACR3   
 A;Cross-references: GDB:9599126   
 C;Superfamily: neurokinin 1 receptor   
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein   
 F;1-111/Domain: transmembrane #status predicted <TM1>   
 F;12-147/Domain: transmembrane #status predicted <TM2>   
 F;160-181/Domain: transmembrane #status predicted <TM3>   
 F;202-221/Domain: transmembrane #status predicted <TM4>   
 F;247-272/Domain: transmembrane #status predicted <TM5>   
 F;330-321/Domain: transmembrane #status predicted <TM6>   
 F;335-355/Domain: transmembrane #status predicted <TM7>   
 F;42-50, 73/Binding site: carbohydrate (Asn) (covalent) #status predicted   
 F;158-233/Disulfide bonds: #status predicted   
 - Query Match 92.1%; Score 105; DB 1; Length 465;   
 - Best Local Similarity 87.0%; Pred. No. 2.9e-09;   
 - Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;   
 - Qy 1 NYFLVNLAFASMAAFNTVNF 23   
 - Db 121 NYFLVNLAFASMAAFNTLNF 143   
 - RESULT 6   
 S55524 neurokinin 3 receptor - mouse (fragment)   
 N;Alternate names: neuropeptide K receptor; NK-3 receptor   
 C;Species: Mus musculus (house mouse)   
 C;Accession: S55524; 173045   
 R;Maroteaux, L.   
 submitted to the EMBL Data Library, June 1995   
 A;Reference number: S55524   
 A;Accession: S55524   
 A;Molecule type: mRNA   
 A;Residues: 1-385 <MAR>   
 A;Cross-references: UNIPROT:P47937; EMBL:X87823; NID:98861055; PIDN:CAA61088.1; PMID:98610   
 R;Cook, G.A.; Elliott, D.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.   
 J. Immunol. 158, 1830-1835, 1994   
 A;Title: Molecular evidence that granuloma T lymphocytes in murine schistosomiasis mansoni   
 A;Reference number: 156216; MUID:94165478; PMID:8120392   
 A;Accession: 173045   
 A;Status: preliminary; translated from GB/EMBL/DDJB   
 N;Alternate names: neurokinin A receptor; NK-2 receptor; substance K receptor (SKR)   
 C;Species: Bos primigenius taurus (cattle)



Db 69 NYFIINLLADLCMAAFNATNFN 91

A;Experimental source: strain Bristol N2; clone C49A9

C;Gene: CESP:C49A9.7

A;Map position: 4

A;Intron: 21/3; 81/2; 128/2; 159/2; 199/3; 233/2; 263/3; 347/2

C;Superfamily: neurokinin 1 receptor

S20303 neurokinin 2 receptor - mouse

N;Alternate names: neurokinin A receptor; NK-2 receptor; substance K receptor (SKR)

C;Species: Mus musculus (house mouse)

C;Accession: S20303

C;Update: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

R;Sundelin, J.B.; Provedini, D.M.; Wahlestedt, C.R.; Laurell, H.; Pohl, J.S.; Pettersson, E.; J. Biochem. 201, 625-631, 1992

A;Title: Molecular cloning of the murine substance K and substance P receptor genes.

A;Reference number: S20303; MUID:92137253; PMID:1137937

A;Accession: S20303

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-384 &lt;SUN&gt;

A;Cross-references: UNIPROT:P30549; GB:X622933; NID:954204; PID:CAA44706.1; PMID:954205

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Score 68.4%; Score 78; DB 2; Length 384;

\*Best Local Similarity 60.9%; Pred. No. 6.1e-05;

Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db

91 NYFIINLLADLCMAAFNATNFN 91

RESULT 14

A36737 neurokinin 2 receptor - rat

N;Alternate names: neurokinin A receptor; NK-2 receptor; substance K receptor (SKR)

C;Species: Rattus norvegicus (Norway rat)

C;Accession: A36737

C;Update: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004

R;Sasai, Y.; Nakaniishi, S.

Biochem. Biophys. Res. Commun. 165, 695-702, 1989

A;Title: Molecular characterization of rat substance K receptor and its mRNAs.

A;Reference number: A36737; MUID:90088481; PMID:2480781

A;Accession: A36737

A;Molecule type: mRNA

A;Residues: 1-390 &lt;SAS&gt;

A;Cross-references: UNIPROT:P16610; GB:M31838; NID:9206986; PID:AAA442150.1; PMID:g206987

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match

Score 68.4%; Score 78; DB 2; Length 390;

\*Best Local Similarity 60.9%; Pred. No. 6.2e-05;

Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db

91 NYFIINLLADLCMAAFNATNFN 91

RESULT 15

T32517 hypothetical protein C49A9.7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Accession: T32517

R;Fulton, B.; Wohlgemann, P.

Submitted to the EMBL Data Library, December 1997

A;Description: The sequence of C. elegans cosmid C49A9.

A;Reference number: Z21184

A;Accession: T32517

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residue: 1-391 &lt;PUL&gt;

A;Cross-references: UNIPROT:O41148; EMBL:AF036693; PIDN:AAB88331.1; GSPDB:GN00022; CBSP:

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